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## Channing Microbiome Seminar September 23<sup>th</sup> (Friday), 2022, 9-10AM (ET)

Zoom: <https://us02web.zoom.us/j/81070959105?pwd=RFJNd3dSZmR6dXJZnJiYVZzQ3NEQT09>

Meeting ID: 810 7095 9105

Passcode: 984617



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## Cross-feeding networks, diauxic shifts, and stable marriage in the human gut microbiome

**Abstract:** The human gut microbiome is a complex ecosystem, in which hundreds of microbial species and metabolites coexist, in part due to an extensive network of cross-feeding interactions. To understand the metabolic flow in such multi-level trophic ecosystems we studied a model where microbes consume and secrete metabolites in multiple iterative steps. This model allowed us to predict the metabolic environment of the gut from its microbial composition [1] and even to reconstruct some of the previously unknown cross-feeding links between species [2].

Another property of the human gut is that the nutrients are typically supplied in discrete batches. Under these conditions many microbes grow diauxically, utilizing the available resources one at a time rather than simultaneously. We developed and studied several models of assembly of diauxically-growing microbial communities [3,4]. We find that complementary resource preferences naturally arise in these communities. That is to say, the surviving species tend to have different resources as their top nutrient choice. The game theoretical approach used in some of our models [4,5] was inspired by a decades-old economics work: the stable marriage or stable allocation problem, developed by Gale and Shapley in the 1960s and awarded the Nobel prize in economics in 2012.

1. Wang T, Goyal A, Dubinkina V, Maslov S. Evidence for a multi-level trophic organization of the human gut microbiome. *PLoS Comp Biol*, 2019, 15(12): e1007524. <https://doi.org/10.1371/journal.pcbi.1007524>
2. Goyal A, Wang T, Dubinkina V, Maslov S. Ecology-guided prediction of cross-feeding interactions in the human gut microbiome. *Nature Communications*, 2021, 12, 1335. <https://doi.org/10.1038/S41467-021-21586-6>.

3. Wang Z, Goyal A, Dubinkina V, George A, Wang T, Fridman Y, Maslov S. Complementary resource preferences spontaneously emerge in diauxic microbial communities. **Nature Communications**, 2021, 12, 6661:6661-6612, <https://www.nature.com/articles/s41467-021-27023-y>
4. Goyal A, Dubinkina V, Maslov S. Microbial community structure predicted by the stable marriage problem. **ISME Journal**, 2018, 12: 2823–2834. <https://doi.org/10.1038/s41396-018-0222-x>
5. Dubinkina V, Fridman Y, Pandey PP, Maslov S. Multistability and regime shifts in microbial communities explained by competition for essential nutrients. **eLife**, 2018, 8:e49720; : <https://doi.org/10.7554/eLife.49720>.

**Bio:** Dr. Maslov is a professor in the department of Bioengineering and Physics at University of Illinois Urbana-Champaign. He received his Ph.D. in Theoretical Statistical Physics from Stony Brook University and did his postdoctoral training at Brookhaven National Laboratory. His current research focuses on the computational modeling of complex biological systems with particular emphasis on dynamics of microbial ecosystems, evolution of bacterial genomes, and complex biomolecular networks (PPI, regulatory, metabolic, food webs). He is also interested in applying machine learning techniques to personalized prediction of cancer drug combinations, predicting transcriptional regulatory networks, gene expression in non-model yeast species, and other microbiome-related projects.

Hosted by Tong Wang & Yang-Yu Liu